



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
- (ii) TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
- (iii) NUMBER OF SEQUENCES: 140
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 - (B) STREET: 130 Water Street
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/776,971
 - (B) FILING DATE: 07-FEB-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/JP96/03821
 - (B) FILING DATE: 28-DEC-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 7/343371
 - (B) FILING DATE: 28-DEC-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 8/59419
 - (B) FILING DATE: 15-MAR-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 8/211805
 - (B) FILING DATE: 12-AUG-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 8/246573
 - (B) FILING DATE: 18-SEP-1996
- (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Conlin, David G.
(B) REGISTRATION NUMBER: 27,026
(C) REFERENCE/DOCKET NUMBER: 47176

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-523-3400
(B) TELEFAX: 617-523-6440

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Lys	Ala	Val	Gly	Ala	Trp	Leu	Leu	Cys	Leu	Leu	Leu	Leu	Gly	Leu
1				5				10						15	
Ala	Leu	Gln	Gly	Ala	Ala	Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile
		20					25					30			
Arg	Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg
		35				40						45			
Pro	Val	Gly	Arg	Phe	Gly	Arg	Arg	Ala	Ala	Pro	Gly	Asp	Gly	Pro	
	50					55				60					
Arg	Pro	Gly	Pro	Arg	Arg	Val	Pro	Ala	Cys	Phe	Arg	Leu	Glu	Gly	Gly
65				70					75					80	
Ala	Glu	Pro	Ser	Arg	Ala	Leu	Pro	Gly	Arg	Leu	Thr	Ala	Gln	Leu	Val
				85				90						95	
Gln	Glu														

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG	60
GCTGCCAGCA	GAGCCACCA	GCACTCCATG	GAGATCCGCA	CCCCGACAT	CAACCCTGCC	120
TGGTACGCRG	GCCGTGGGAT	CCGGCCCGTG	GGCCGCTTCG	CCCGGCGAAG	AGCTGCCCCY	180
GGGGACGGAC	CCAGGCCTGG	CCCCCGGCGT	GTGCCGCGCT	GCTTCCGCCT	GGAAGGCGGY	240
GCTGAGCCCT	CCCAGCCCT	CCCGGGGCGG	CTGACGGCCC	AGCTGGTCCA	GGAA	294

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly			
			20					25							

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro
1				5					10					15	
Val	Gly	Arg													

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
			20					25						30	

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
			20					25						30	

Arg

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
 1 5 10 15
 Val Gly Arg Phe
 20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
 1 5 10 15
 Val Gly Arg Phe Gly
 20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
 1 5 10 15
 Val Gly Arg Phe Gly Arg
 20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC
GCRGGCCGTG GGATCCGGCC CGTGGGC

60
87

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCCGT GGGCCGC

57

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC
GCRGGCCGTG GGATCCGGCC CGTGGGCCGC TTC

60
93

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC
GCRGGCCGTG GGATCCGGCC CGTGGGCCGC TTCGGC

60
96

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC	60
GCRGGCCGTG GGATCCGGCC CGTGGGCCGC TTCGGCCGG	99

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGCTTC	60
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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGCTTC	60
GGC	63

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGCTTC	60
GGCCGG	66

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn
1          5          10          15
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
          20          25          30
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
          35          40          45
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
          50          55          60
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
65          70          75          80
Val Val Leu Val His Pro Leu Arg Arg Arg Ile
          85          90
```

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu
1          5          10          15
Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly
          20          25          30
Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg
          35          40          45
Thr Phe Cys Leu Leu Val Val Val Val Val Val
50          55
```

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Ala	Ser	Ser	Thr	Thr	Arg	Gly	Pro	Arg	Val	Ser	Asp	Leu	Phe	Ser
1				5					10					15	
Gly	Leu	Pro	Pro	Ala	Val	Thr	Thr	Pro	Ala	Asn	Gln	Ser	Ala	Glu	Ala
			20					25					30		
Ser	Ala	Gly	Asn	Gly	Ser	Val	Ala	Gly	Ala	Asp	Ala	Pro	Ala	Val	Thr
		35					40					45			
Pro	Phe	Gln	Ser	Leu	Gln	Leu	Val	His	Gln	Leu	Lys	Gly	Leu	Ile	Val
	50					55				60					
Leu	Leu	Tyr	Ser	Val	Val	Val	Val	Val	Gly	Leu	Val	Gly	Asn	Cys	Leu
65				70						75				80	
Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg	Leu	His	Asn	Val	Thr	Asn
				85					90					95	
Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	Met	Cys	Thr	Ala
			100					105					110		
Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val
		115					120					125			
Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr
	130					135					140				
Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr
145				150						155				160	
Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser
				165					170					175	
Ala	Tyr	Ala	Val	Leu	Ala	Ile	Trp	Ala	Leu	Ser	Ala	Val	Leu	Ala	Leu
			180					185					190		
Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val
	195						200					205			
Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu
	210					215					220				
Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Val	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Val
225				230						235				240	
Ile	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val
				245					250					255	
Val	Pro	Gly	Cys	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg
			260					265					270		
Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Ala
		275					280					285			
Val	Cys	Trp	Leu	Pro	Leu	His	Val	Phe	Asn	Leu	Leu	Arg	Asp	Leu	Asp
	290					295				300					
Pro	His	Ala	Ile	Asp	Pro	Tyr	Ala	Phe	Gly	Leu	Val	Gln	Leu	Leu	Cys
305				310						315				320	
His	Trp	Leu	Ala	Met	Ser	Ser	Ala	Cys	Tyr	Asn	Pro	Phe	Ile	Tyr	Ala
				325					330					335	
Trp	Leu	His	Asp	Ser	Phe	Arg	Glu	Glu	Leu	Arg	Lys	Leu	Leu	Val	Ala
			340					345							

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu Tyr Asn Val Thr Asn
1          5          10          15
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
20          25          30
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
35          40          45
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr
50          55          60
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
65          70          75          80
Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser
85          90          95
Ala Tyr Ala Val Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu
100          105          110
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
115          120          125
Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
130          135          140
Tyr Ala Trp Gly Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
145          150          155          160
Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val
165          170          175
Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
180          185          190
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val
195          200          205

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser
1				5					10					15	
Ala	Tyr	Ala	Val	Leu	Gly	Ile	Trp	Ala	Leu	Ser	Ala	Val	Leu	Ala	Leu
			20					25					30		
Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val
			35				40					45			
Ser	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Ile
	50					55				60					
Tyr	Ala	Trp	Gly	Leu	Leu	Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala	
65					70				75					80	
Ile	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val
				85				90					95		
Val	Pro	Gly	Ser	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg
			100				105						110		
Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Val	
		115					120						125		

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGGTGCTGG	TGATCGCGCG	GGTGCGCCGG	CTGCACAACG	TGACGAACTT	CCTCATCGGC	60
AACCTGGCCT	TGTCCGACGT	GCTCATGTGC	ACCGCCTGCG	TGCCGCTCAC	GCTGGCCTAT	120
GCCTTCGAGC	CACGCGGCTG	GGTGTTCGGC	GGCGGCCTGT	GCCACCTGGT	CTTCTTCCTG	180
CAGCCGGTCA	CCGTCTATGT	GTCGGTGTTC	ACGCTCACCA	CCATCGCAGT	GGACCGGTAC	240
GTCGTGCTGG	TGCACCCGCT	GAGGCGGCGC	ATC			273

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGCCTGCTGC	TGGTCACCTA	CCTGCTCCCT	CTGCTGGTCA	TCCTCCTGTC	TTACGTCCGG	60
GTGTCAAGTA	AGCTCCGCAA	CCGCGTGGTG	CCGGGCTGCG	TGACCCAGAG	CCAGGCCGAC	120
TGGGACCGCG	CTCGGCGCCG	GCGCACCTTC	TGCTTGCTGG	TGGTGGTCGT	GGTGGTG	177

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGGCCTCAT	CGACCACTCG	GGGCCCCAGG	GTTTCTGACT	TATTTTCTGG	GCTGCCGCCG	60
GCGGTCACAA	CTCCCCCAA	CCAGAGCGCA	GAGGCCTCGG	CGGGCAACGG	GTCGGTGGCT	120
GGCGCGGACG	CTCAGCCGT	CACGCCCTTC	CAGAGCCTGC	AGCTGGTGCA	TCAGCTGAAG	180
GGGCTGATCG	TGCTGCTCTA	CAGCGTCGTG	GTGGTCGTGG	GGCTGGTGGG	CAACTGCCTG	240
CTGGTGCTGG	TGATCGCGCG	GGTGCGCCGG	CTGCACAACG	TGACGAACTT	CCTCATCGGC	300
AACCTGGCCT	TGTCCGACGT	GCTCATGTGC	ACCGCCTGCG	TGCCGCTCAC	GCTGGCCTAT	360
GCCTTCGAGC	CACGCGGCTG	GGTGTTCGGC	GGCGGCCTGT	GCCACCTGGT	CTTCTTCCTG	420
CAGCCGGTCA	CCGTCTATGT	GTCGGTGTTT	ACGCTCACCA	CCATCGCAGT	GGACCGCTAC	480
GTCGTGCTGG	TGCACCCGCT	GAGGCGGCGC	ATCTCGCTGC	GCCTCAGCGC	CTACGCTGTG	540
CTGGCCATCT	GGGCGCTGTC	CGCGGTGCTG	GCGCTGCCCG	CCGCCGTGCA	CACCTATCAC	600
GTGGAGCTCA	AGCCGCACGA	CGTGCGCCTC	TGCGAGGAGT	TCTGGGGCTC	CCAGGAGCGC	660
CAGCGCCAGC	TCTACGCCTG	GGGGCTGCTG	CTGGTCACCT	ACCTGCTCCC	TCTGCTGGTC	720
ATCCTCCTGT	CTTACGTCCG	GGTGTCAAGT	AAGCTCCGCA	ACCGCGTGGT	GCCGGGCTGC	780
GTGACCCAGA	GCCAGGCCGA	CTGGGACCGC	GCTCGGCGCC	GGCGCACCTT	CTGCTTGCTG	840
GTGGTGCTCG	TGGTGCTGTT	CGCCGTCTGC	TGGCTGCCGC	TGCACGTCTT	CAACCTGCTG	900
CGGGACCTCG	ACCCACACGC	CATCGACCCT	TACGCCTTTG	GGCTGGTGCA	GCTGCTCTGC	960
CACTGGCTCG	CCATGAGTTC	GGCCTGCTAC	AACCCCTTCA	TCTACGCCTG	GCTGCACGAC	1020
AGCTTCCGCG	AGGAGCTGCG	CAAAGTGTG	GTCGCTTGGC	CCCGCAAGAT	AGCCCCCAT	1080
GGCCAGAATA	TGACCGTCAG	CGTGGTCATC				1110

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 618 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGGTGCTGG	TGATCGCGCG	GGTGCGCCGG	CTGTACAACG	TGACGAATTT	CCTCATCGGC	60
AACCTGGCCT	TGTCCGACGT	GCTCATGTGC	ACCGCCTGCG	TGCCGCTCAC	GCTGGCCTAT	120
GCCTTCGAGC	CACGCGGCTG	GGTGTTCGGC	GGCGGCCTGT	GCCACCTGGT	CTTCTTCCTG	180
CAGGCGGTCA	CCGTCTATGT	GTCGGTGTTT	ACGCTCACCA	CCATCGCAGT	GGACCGCTAC	240
GTCGTGCTGG	TGCACCCGCT	GAGGCGGCGC	ATCTCGCTGC	GCCTCAGCGC	CTACGCTGTG	300
CTGGCCATCT	GGGTGCTGTC	CGCGGTGCTG	GCGTGCCCG	CCGCCGTGCA	CACCTATCAC	360
GTGGAGCTCA	AGCCGCACGA	CGTGCGCCTC	TGCGAGGAGT	TCTGGGGCTC	CCAGGAGCGC	420
CAGCGCCAGC	TCTACGCCTG	GGGGCTGCTG	CTGGTCACCT	ACCTGCTCCC	TCTGCTGGTC	480
ATCCTCCTGT	CTTACGCCCG	GGTGTCAAGT	AAGCTCCGCA	ACCGCGTGGT	GCCGGGCCGC	540
GTGACCCAGA	GCCAGGCCGA	CTGGGACCGC	GCTCGGCGCC	GGCGCACCTT	CTGCTTGCTG	600
GTGGTGCTCG	TGGTGCTG					618

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTGGTTCTGG	TGCACCCGCT	ACGTCGGCGC	ATTTCACTGA	GGCTCAGCGC	CTACGCGGTG	60
CTGGGCATCT	GGGCTCTATC	TGCAGTGCTG	GCGCTGCCGG	CCGCGGTGCA	CACCTACCAT	120
GTGGAGCTCA	AGCCCCACGA	CGTGAGCCTC	TGCGAGGAGT	TCTGGGGCTC	GCAGGAGCGC	180
CAACGCCAGA	TCTACGCCTG	GGGGCTGCTT	CTGGGCACCT	ATTTGCTCCC	CCTGCTGGCC	240
ATCCTCCTGT	CTTACGTACG	GGTGTCAGTG	AAGCTGAGGA	ACCGCGTGGT	GCCTGGCAGC	300
GTGACCCAGA	GTCAAGCTGA	CTGGGACCGA	GCGCGTCGCC	GCCGCACTTT	CTGTCTGCTG	360
GTGGTGGTGG	TGGTAGTG					378

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGTGGSCMTS	STGGGCAACN	YCCTG	25
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(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTNGWRRGGC	ANCCAGCAGA	KGGCAAA	27
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(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGTGYGYSA TYGCNNTKGA YMGSTAC

27

- (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AKGWAGWAGG GCAGCCAGCA GANSRYGAA

29

- (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGACTTATT TTCTGGGCTG CCGC

24

- (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /mod_base= i.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCNCAYCARC AYTGYATGGA

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 15
 - (D) OTHER INFORMATION: /mod_base= i
- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 21
 - (D) OTHER INFORMATION: /mod_base= i
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ACGGGCCCKDA TGCCNCKGCC NGCRTA

26

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCGGCGTACC AGGCAGGGTT

20

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGGCAGGGTT GATGTCGGGG GTGCGGAT

28

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGCCAGCAG AGCCCACCAG CACTCCA

27

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGGGGGCCT GGCTCCTCTG CCTGCTG

27

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTGTCGACGA ATGAAGGCGG TGGGGGCCTG GC

32

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGGCTCCCGC TGTTATTCCT GGAC

24

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear .

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Lys	Ala	Val	Gly	Ala	Trp	Leu	Leu	Cys	Leu	Leu	Leu	Gly	Leu	
1				5				10					15		
Ala	Leu	Gln	Gly	Ala	Ala	Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile
		20						25					30		
Arg	Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg
		35					40					45			
Pro	Val	Gly	Arg	Phe	Gly	Arg	Arg	Arg	Ala	Ala	Leu	Gly	Asp	Gly	Pro
		50				55					60				
Arg	Pro	Gly	Pro	Arg	Arg	Val	Pro	Ala	Cys	Phe	Arg	Leu	Glu	Gly	Gly
65				70					75					80	
Ala	Glu	Pro	Ser	Arg	Ala	Leu	Pro	Gly	Arg	Leu	Thr	Ala	Gln	Leu	Val
				85					90					95	
Gln	Glu														

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Ala	Leu	Lys	Thr	Trp	Leu	Leu	Cys	Leu	Leu	Leu	Ser	Leu	Val	
1				5				10				15			
Leu	Pro	Gly	Ala	Ser	Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Thr	Arg

[illegible]

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEO ID NO:46:

ATGGCCCTGA	AGACGTGGCT	TCTGTGCTTG	CTGCTGCTAA	GCTTGGTCCCT	CCCAGGGGGCT	60
TCCAGCCGAG	CCCACCAGCA	CTCCATGGAG	ACAAGAACCC	CTGATATCAA	TCCTGCCTGG	120
TACACGGGCC	GCGGGATCAG	GCCTGTGGGC	CGCTTCGGCA	GGAGAAGGGC	AACCCCAGAG	180
GATGTCACTG	GACTTGGCCA	ACTCAGCTGC	CTCCCACTGG	ATGGACGCAC	CAAGTTCTCT	240
CAGCGTGGG						249

(2) INFORMATION FOR SEO ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEO ID NO:47:

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Thr	Arg	Thr	Pro	Asp	Ile	Asn
1			5					10					15		
Pro	Ala	Trp	Tyr	Thr	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
		20					25					30			

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Thr	Arg	Thr	Pro	Asp	Ile	Asn
1			5					10					15		
Pro	Ala	Trp	Tyr	Thr	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
		20					25					30			

Arg

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Thr	Gly	Arg	Gly	Ile	Arg	Pro
1			5					10					15		
Val	Gly	Arg	Phe												
		20													

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
1           5           10           15
Val Gly Arg Phe Gly
                20

```

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
1           5           10           15
Val Gly Arg Phe Gly Arg
                20

```

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAACCCCTG ATATCAATCC TGCCTGGTAC 60
ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTC 93

```

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAACCCCTG ATATCAATCC TGCCTGGTAC	60
ACGGGCCCGCG GGATCAGGCC TGTGGGCCGC TTCGGC	96

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAACCCCTG ATATCAATCC TGCCTGGTAC	60
ACGGGCCCGCG GGATCAGGCC TGTGGGCCGC TTCGGCAGG	99

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC	60
---	----

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC	60
GGC	63

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC
GGCAGG

60

66

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met	Lys	Val	Leu	Arg	Ala	Trp	Leu	Leu	Cys	Leu	Leu	Met	Leu	Gly	Leu
1			5					10						15	
Ala	Leu	Arg	Gly	Ala	Ala	Ser	Arg	Thr	His	Arg	His	Ser	Met	Glu	Ile
		20					25					30			
Arg	Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg
		35				40					45				
Pro	Val	Gly	Arg	Phe	Gly	Arg	Arg	Arg	Ala	Thr	Leu	Gly	Asp	Val	Pro
	50				55				60						
Lys	Pro	Gly	Leu	Arg	Pro	Arg	Leu	Thr	Cys	Phe	Pro	Leu	Glu	Gly	Gly
65				70					75					80	
Ala	Met	Ser	Ser	Gln	Asp	Gly									
				85											

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGAAGGTGC	TGAGGGCCTG	GCTCCTGTGC	CTGCTGATGC	TGGGCCTGGC	CCTGCGGGGA	60
GCTGCAAGTC	GTACCCATCG	GCACTCCATG	GAGATCCGCA	CCCCTGACAT	CAATCCTGCC	120
TGGTACGCCA	GTCGCGGGAT	CAGGCCTGTG	GGCCGCTTCG	GTCGGAGGAG	GGCAACCCTG	180
GGGGACGTCC	CCAAGCCTGG	CCTGCGACCC	CGGCTGACCT	GCTTCCCCCT	GGAAGGCGGT	240
GCTATGTCGT	CCCAGGATGG	C				261

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ser	Arg	Thr	His	Arg	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1			5					10						15	
Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	
		20					25					30			

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ser	Arg	Thr	His	Arg	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1			5					10						15	
Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
		20					25					30			

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
 20 25 30
Arg

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe
 20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe Gly
 20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro
1				5				10					15		
Val	Gly	Arg	Phe	Gly	Arg										
			20												

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

AGTCGTACCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC	60
GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTC	93

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGTCGTACCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC	60
GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTCGGT	96

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AGTCGTACCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC 60
GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTCGGTCGG 99

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60
GGT 63

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60
GGTCGG 66

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "Ala or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /product= "Gly or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 21..22
(D) OTHER INFORMATION: /product= "may be a Gly-Arg or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Xaa	Xaa	Arg	Gly	Ile	Arg	Pro
1			5				10				15				
Val	Gly	Arg	Phe	Xaa	Xaa										
			20												

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /product= "Ala or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "Gln or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "Ile or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Arg Xaa His Xaa His Ser Met Glu Xaa Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CARCAYTCCA TGGAGACAAG AACCCC

26

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TACCAGGCAG GATTGATACA GGGG

24

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCATCATCC AGGAAGACGG AGCAT

25

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AGCAGAGGAG AGGGAGGGTA GAGGA

25

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ACGTGGCTTC TGTGCTTGCT GC

22

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GCCTGATCCC GCGGCCCGTG TACCA

25

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTGCCCTTCT CCTGCCGAAG CGGCCC

26

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGCGGGGGCT GCAAGTCGTA CCCATCG

27

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CGGCACTCCA TGGAGATCCG CACCCCT

27

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGGCAGGAT TGATGTCAGG GGTGCGG

27

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CATGGAGTGC CGATGGGTAC GACTTGC

27

- (2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGCCTCCTCG GAGGAGCCAA GGGATGA

27

- (2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGGAAAGGAG CCCGAAGGAG AGGAGAG

27

- (2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CCTGCTGGCC ATTCTCCTGT CTTAC

25

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GGGTCCAGGT CCCGCAGAAG GTTGA

25

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GAAGACGGAG CATGGCCCTG AAGAC

25

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCAGCTGAG TTGGCCAAGT CCACT

25

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Cys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Cys	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Cys	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Gly
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTTACACAGGT CGACATGACC TCAC

24

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTCAGAGCTA GCAGAGTGTC ATCAG

25

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser	Arg	Ala	His	Gln	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Gly	Arg	Gly	Ile	Arg	Pro
1				5					10				15		
Val	Gly	Arg	Phe												
			20												

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...669
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTG GGC ATG GTG GGC AAC ATC CTG CTG GTG CTG GTG ATC GCG CGG GTG	48
Val Gly Met Val Gly Asn Ile Leu Leu Val Leu Val Ile Ala Arg Val	
1 5 10 15	
CGC CGG CTG TAC AAC GTG ACG AAT TTC CTC ATC GGC AAC CTG GCC TTG	96
Arg Arg Leu Tyr Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu	
20 25 30	
TCC GAC GTG CTC ATG TGC ACC GCC TGC GTG CCG CTC ACG CTG GCC TAT	144
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr	
35 40 45	
GCC TTC GAG CCA CGC GGC TGG GTG TTC GGC GGC GGC CTG TGC CAC CTG	192
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu	
50 55 60	
GTC TTC TTC CTG CAG GCG GTC ACC GTC TAT GTG TCG GTG TTC ACG CTC	240
Val Phe Phe Leu Gln Ala Val Thr Val Tyr Val Ser Val Phe Thr Leu	
65 70 75 80	
ACC ACC ATC GCA GTG GAC CGC TAC GTC GTG CTG GTG CAC CCG CTG AGG	288
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg	
85 90 95	
CGG CGC ATC TCG CTG CGC CTC AGC GCC TAC GCT GTG CTG GCC ATC TGG	336
Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Ala Ile Trp	
100 105 110	
GTG CTG TCC GCG GTG CTG GCG CTG CCC GCC GCC GTG CAC ACC TAT CAC	384
Val Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr His	
115 120 125	
GTG GAG CTC AAG CCG CAC GAC GTG CGC CTC TGC GAG GAG TTC TGG GGC	432
Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly	
130 135 140	
TCC CAG GAG CGC CAG CGC CAG CTC TAC GCC TGG GGG CTG CTG CTG GTC	480
Ser Gln Glu Arg Gln Arg Gln Leu Tyr Ala Trp Gly Leu Leu Leu Val	
145 150 155 160	
ACC TAC CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC GCC CGG GTG	528
Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr Ala Arg Val	
165 170 175	

TCA GTG AAG CTC CGC AAC CGC GTG GTG CCG GGC CGC GTG ACC CAG AGC	576
Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Arg Val Thr Gln Ser	
180 185 190	

CAG GCC GAC TGG GAC CGC GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG	624
Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Thr Phe Cys Leu Leu	
195 200 205	

GTG GTG GTC GTG GTG GTG TTC ACC CTC TGC TGG CTG CCC TTC TTC	669
Val Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Phe	
210 215 220	

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Gly Met Val Gly Asn Ile Leu Leu Val Leu Val Ile Ala Arg Val	
1 5 10 15	
Arg Arg Leu Tyr Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu	
20 25 30	
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr	
35 40 45	
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu	
50 55 60	
Val Phe Phe Leu Gln Ala Val Thr Val Tyr Val Ser Val Phe Thr Leu	
65 70 75 80	
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg	
85 90 95	
Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Ala Ile Trp	
100 105 110	
Val Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr His	
115 120 125	
Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly	
130 135 140	
Ser Gln Glu Arg Gln Arg Gln Leu Tyr Ala Trp Gly Leu Leu Leu Val	
145 150 155 160	
Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr Ala Arg Val	
165 170 175	
Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Arg Val Thr Gln Ser	
180 185 190	
Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Thr Phe Cys Leu Leu	
195 200 205	
Val Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Phe	
210 215 220	

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val
1 5 10 15
Arg Arg Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu
20 25 30
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr
35 40 45
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu
50 55 60
Val Phe Phe Leu Gln Pro Val Thr Val Tyr Val Ser Val Phe Thr Leu
65 70 75 80
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg
85 90 95
Arg Arg Ile Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
100 105 110
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
115 120 125
Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
130 135 140
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala
145 150 155 160
Ile Cys Trp Leu Pro Tyr Tyr
165

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val Gly Met Val Gly Asn Ile Leu Leu Val Leu Val Ile Ala Arg Val
1 5 10 15
Arg Arg Leu Tyr Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu
20 25 30
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr
35 40 45
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu
50 55 60
Val Phe Phe Leu Gln Ala Val Thr Val Tyr Val Ser Val Phe Thr Leu
65 70 75 80
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg
85 90 95
Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Ala Ile Trp

Val	Leu	Ser	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr	His
	115						120					125			
Val	Glu	Leu	Lys	Pro	His	Asp	Val	Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly
	130					135				140					
Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Val
145				150				155						160	
Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Val	Ile	Leu	Leu	Ser	Tyr	Ala	Arg	Val
			165					170						175	
Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly	Arg	Val	Thr	Gln	Ser
		180					185						190		
Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu
	195					200					205				
Val	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Phe	
210						215					220				

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 118...1227
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CATCGTCAAG	CAGATGAAGA	TCATCCACGA	GGATGGCTAC	TCCGAGGGCC	AGCAGAAATT	60
CTGCCCTTC	TTCCCGCGAG	TGCTTTCCCG	CTCTCCAAAC	CCCACTCCCA	GGTGGCC ATG	120
					Met	
					1	
GCC TCA TCG ACC ACT CGG GGC CCC AGG GTT TCT GAC TTA TTT TCT GGG	168					
Ala Ser Ser Thr Thr Arg Gly Pro Arg Val Ser Asp Leu Phe Ser Gly						
5 10 15						
CTG CCG CCG GCG GTC ACA ACT CCC GCC AAC CAG AGC GCA GAG GCC TCG	216					
Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala Ser						
20 25 30						
GCG GGC AAC GGG TCG GTG GCT GGC GCG GAC GCT CCA GCC GTC ACG CCC	264					
Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr Pro						
35 40 45						
TTC CAG AGC CTG CAG CTG GTG CAT CAG CTG AAG GGG CTG ATC GTG CTG	312					
Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val Leu						
50 55 60 65						
CTC TAC AGC GTC GTG GTG GTC GTG GGG CTG GTG GGC AAC TGC CTG CTG	360					
Leu Tyr Ser Val Val Val Val Val Gly Leu Val Gly Asn Cys Leu Leu						
70 75 80						

GTG	CTG	GTG	ATC	GCG	CGG	GTG	CGC	CGG	CTG	CAC	AAC	GTG	ACG	AAC	TTC	408
Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Arg	Leu	His	Asn	Val	Thr	Asn	Phe	
			85					90					95			
CTC	ATC	GGC	AAC	CTG	GCC	TTG	TCC	GAC	GTG	CTC	ATG	TGC	ACC	GCC	TGC	456
Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	Met	Cys	Thr	Ala	Cys	
		100					105					110				
GTG	CCG	CTC	ACG	CTG	GCC	TAT	GCC	TTC	GAG	CCA	CGC	GGC	TGG	GTG	TTC	504
Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val	Phe	
	115					120					125					
GGC	GGC	GGC	CTG	TGC	CAC	CTG	GTC	TTC	TTC	CTG	CAG	CCG	GTC	ACC	GTC	552
Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr	Val	
130					135					140					145	
TAT	GTG	TCG	GTG	TTC	ACG	CTC	ACC	ACC	ATC	GCA	GTG	GAC	CGC	TAC	GTC	600
Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val	
				150					155					160		
GTG	CTG	GTG	CAC	CCG	CTG	AGG	CGG	CGC	ATC	TCG	CTG	CGC	CTC	AGC	GCC	648
Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	
			165					170					175			
TAC	GCT	GTG	CTG	GCC	ATC	TGG	GCG	CTG	TCC	GCG	GTG	CTG	GCG	CTG	CCC	696
Tyr	Ala	Val	Leu	Ala	Ile	Trp	Ala	Leu	Ser	Ala	Val	Leu	Ala	Leu	Pro	
		180					185					190				
GCC	GCC	GTG	CAC	ACC	TAT	CAC	GTG	GAG	CTC	AAG	CCG	CAC	GAC	GTG	CGC	744
Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val	Arg	
	195					200					205					
CTC	TGC	GAG	GAG	TTC	TGG	GGC	TCC	CAG	GAG	CGC	CAG	CGC	CAG	CTC	TAC	792
Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu	Tyr	
210					215					220					225	
GCC	TGG	GGG	CTG	CTG	CTG	GTC	ACC	TAC	CTG	CTC	CCT	CTG	CTG	GTC	ATC	840
Ala	Trp	Gly	Leu	Leu	Leu	Val	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Val	Ile	
				230					235					240		
CTC	CTG	TCT	TAC	GTC	CGG	GTG	TCA	GTG	AAG	CTC	CGC	AAC	CGC	GTG	GTG	888
Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	
			245					250					255			
CCG	GGC	TGC	GTG	ACC	CAG	AGC	CAG	GCC	GAC	TGG	GAC	CGC	GCT	CGG	CGC	936
Pro	Gly	Cys	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	
		260					265					270				
CGG	CGC	ACC	TTC	TGC	TTG	CTG	GTG	GTG	GTC	GTG	GTG	GTG	TTC	GCC	GTC	984
Arg	Arg	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Ala	Val	
	275					280					285					
TGC	TGG	CTG	CCG	CTG	CAC	GTC	TTC	AAC	CTG	CTG	CGG	GAC	CTC	GAC	CCC	1032
Cys	Trp	Leu	Pro	Leu	His	Val	Phe	Asn	Leu	Leu	Arg	Asp	Leu	Asp	Pro	
290					295					300					305	

CAC GCC ATC GAC CCT TAC GCC TTT GGG CTG GTG CAG CTG CTC TGC CAC	1080
His Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys His	
310 315 320	
TGG CTC GCC ATG AGT TCG GCC TGC TAC AAC CCC TTC ATC TAC GCC TGG	1128
Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala Trp	
325 330 335	
CTG CAC GAC AGC TTC CGC GAG GAG CTG CGC AAA CTG TTG GTC GCT TGG	1176
Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Leu Leu Val Ala Trp	
340 345 350	
CCC CGC AAG ATA GCC CCC CAT GGC CAG AAT ATG ACC GTC AGC GTG GTC	1224
Pro Arg Lys Ile Ala Pro His Gly Gln Asn Met Thr Val Ser Val Val	
355 360 365	
ATC TGATGCCACT TAGCCAGGCC TTGGTCAAGG AGCTCCACTT CAACTGGCCT CCTAGG	1283
Ile.	
370	
GCACCACTCG AGGTCAATCT GGTGCTTATT CTCAGCACCA GAGCTAGC	1331

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met	Ala	Ser	Ser	Thr	Thr	Arg	Gly	Pro	Arg	Val	Ser	Asp	Leu	Phe	Ser
1				5				10						15	
Gly	Leu	Pro	Pro	Ala	Val	Thr	Thr	Pro	Ala	Asn	Gln	Ser	Ala	Glu	Ala
			20					25					30		
Ser	Ala	Gly	Asn	Gly	Ser	Val	Ala	Gly	Ala	Asp	Ala	Pro	Ala	Val	Thr
		35					40					45			
Pro	Phe	Gln	Ser	Leu	Gln	Leu	Val	His	Gln	Leu	Lys	Gly	Leu	Ile	Val
	50				55					60					
Leu	Leu	Tyr	Ser	Val	Val	Val	Val	Gly	Leu	Val	Gly	Asn	Cys	Leu	
65				70				75					80		
Leu	Val	Leu	Val	Ile	Ala	Arg	Val	Arg	Leu	His	Asn	Val	Thr	Asn	
			85					90					95		
Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu	Met	Cys	Thr	Ala
		100						105					110		
Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly	Trp	Val
		115					120					125			
Phe	Gly	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr
	130					135					140				
Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr
145					150					155				160	
Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser

CAT GTG GAG CTC AAG CCC CAC GAC GTG AGC CTC TGC GAG GAG TTC TGG	192
His Val Glu Leu Lys Pro His Asp Val Ser Leu Cys Glu Glu Phe Trp	
50 55 60	
GGC TCG CAG GAG CGC CAA CGC CAG ATC TAC GCC TGG GGG CTG CTT CTG	240
Gly Ser Gln Glu Arg Gln Arg Gln Ile Tyr Ala Trp Gly Leu Leu Leu	
65 70 75 80	
GGC ACC TAT TTG CTC CCC CTG CTG GCC ATC CTC CTG TCT TAC GTA CGG	288
Gly Thr Tyr Leu Leu Pro Leu Leu Ala Ile Leu Leu Ser Tyr Val Arg	
85 90 95	
GTG TCA GTG AAG CTG AGG AAC CGC GTG GTG CCT GGC AGC GTG ACC CAG	336
Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Ser Val Thr Gln	
100 105 110	
AGT CAA GCT GAC TGG GAC CGA GCG CGT CGC CGC CGC ACT TTC TGT CTG	384
Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu	
115 120 125	
CTG GTG GTG GTG GTG GTA GTG TTC ACG CTC TGC TGG CTG CCC TTC TAC C	433
Leu Val Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Tyr	
130 135 140	
T	434

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Leu Cys Val Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu	
1 5 10 15	
Arg Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Gly Ile	
20 25 30	
Trp Ala Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr	
35 40 45	
His Val Glu Leu Lys Pro His Asp Val Ser Leu Cys Glu Glu Phe Trp	
50 55 60	
Gly Ser Gln Glu Arg Gln Arg Gln Ile Tyr Ala Trp Gly Leu Leu Leu	
65 70 75 80	
Gly Thr Tyr Leu Leu Pro Leu Leu Ala Ile Leu Leu Ser Tyr Val Arg	
85 90 95	
Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Ser Val Thr Gln	
100 105 110	
Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Thr Phe Cys Leu	
115 120 125	
Leu Val Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Tyr	

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val
 1           5           10           15
Arg Arg Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu
      20           25           30
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr
      35           40           45
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu
      50           55           60
Val Phe Phe Leu Gln Pro Val Thr Val Tyr Val Ser Val Phe Thr Leu
      65           70           75           80
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg
      85           90           95
Arg Arg Ile Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
      100          105          110
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
      115          120          125
Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
      130          135          140
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala
      145          150          155          160
Ile Cys Trp Leu Pro Tyr Tyr
      165

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Val Gly Met Val Gly Asn Ile Leu Leu Val Leu Val Ile Ala Arg Val
 1           5           10           15
Arg Arg Leu Tyr Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu
      20           25           30
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr
      35           40           45
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu
      50           55           60
Val Phe Phe Leu Gln Ala Val Thr Val Tyr Val Ser Val Phe Thr Leu
      65           70           75           80

```

Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg
				85					90					95	
Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Ala	Ile	Trp
			100					105					110		
Val	Leu	Ser	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr	His
		115					120					125			
Val	Glu	Leu	Lys	Pro	His	Asp	Val	Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly
	130					135				140					
Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Val
145				150					155						160
Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Val	Ile	Leu	Leu	Ser	Tyr	Ala	Arg	Val
			165					170						175	
Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly	Arg	Val	Thr	Gln	Ser
		180					185						190		
Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg	Thr	Phe	Cys	Leu	Leu
	195					200					205				
Val	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Phe	
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Leu	Cys	Val	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu
1				5				10					15		
Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Gly	Ile
			20				25					30			
Trp	Ala	Leu	Ser	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr
	35					40					45				
His	Val	Glu	Leu	Lys	Pro	His	Asp	Val	Ser	Leu	Cys	Glu	Glu	Phe	Trp
	50				55				60						
Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Ile	Tyr	Ala	Trp	Gly	Leu	Leu	Leu
65				70				75						80	
Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala	Ile	Leu	Leu	Ser	Tyr	Val	Arg
			85				90						95		
Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly	Ser	Val	Thr	Gln
		100					105					110			
Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg	Thr	Phe	Cys	Leu
	115					120					125				
Leu	Val	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Tyr
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...75
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GCC CAC CAG CAC TCC ATG GAG ATC CGC ACC CCC GAC ATC AAC CCT GCC 48
Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala
1 5 10 15

TGG TAC GCG GGC CGT GGG ATC CGG CCC G 76
Trp Tyr Ala Gly Arg Gly Ile Arg Pro
20 25

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala  
1 5 10 15  
Trp Tyr Ala Gly Arg Gly Ile Arg Pro  
20 25

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 6...125  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GTGGA ATG AAG GCG GTG GGG GCC TGG CTC CTC TGC CTG CTG CTG CTG GGC 50  
Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly  
1 5 10 15

CTG GCC CTG CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG 98  
 Leu Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu  
                   20                  25                  30

ATC CGC ACC CCC GAC ATC AAC CCT GCC T 126  
 Ile Arg Thr Pro Asp Ile Asn Pro Ala  
                   35                  40

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu  
   1                  5                  10                  15  
 Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile  
                   20                  25                  30  
 Arg Thr Pro Asp Ile Asn Pro Ala  
                   35                  40

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 6...299

(D) OTHER INFORMATION:

(A) NAME/KEY: Modified Base

(B) LOCATION: 43...43

(D) OTHER INFORMATION: Xaa is Ala

(A) NAME/KEY: Modified Base

(B) LOCATION: 80...80

(D) OTHER INFORMATION: Xaa is Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GTGGA ATG AAG GCG GTG GGG GCC TGG CTC CTC TGC CTG CTG CTG CTG GGC 50  
 Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly  
   1                  5                  10                  15

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTG GCC CTG CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG   | 98  |
| Leu Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu   |     |
| 20 25 30                                                          |     |
| ATC CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC GCR GGC CGT GGG ATC   | 146 |
| Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Gly Arg Gly Ile   |     |
| 35 40 45                                                          |     |
| CGG CCC GTG GGC CGC TTC GGC CGG CGA AGA GCT GCC CCG GGG GAC GGA   | 194 |
| Arg Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Pro Gly Asp Gly   |     |
| 50 55 60                                                          |     |
| CCC AGG CCT GGC CCC CGG CGT GTG CCG GCC TGC TTC CGC CTG GAA GGC   | 242 |
| Pro Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly   |     |
| 65 70 75                                                          |     |
| GGY GCT GAG CCC TCC CGA GCC CTC CCG GGG CGG CTG ACG GCC CAG CTG   | 290 |
| Xaa Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu   |     |
| 80 85 90 95                                                       |     |
| GTC CAG GAA TAACAGCGGG AGCCTGCCCC CCACCCCTCC TCCTCCACCA GCCACCTTC | 348 |
| Val Gln Glu                                                       |     |
| CCTCCAGTCC TAATAAAAGC AGCTGGCTTG TT                               | 380 |

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 43...43
- (D) OTHER INFORMATION: Xaa is Ala

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 80...80
- (D) OTHER INFORMATION: Xaa is Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu |  |
| 1 5 10 15                                                       |  |
| Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile |  |
| 20 25 30                                                        |  |
| Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Gly Arg Gly Ile Arg |  |
| 35 40 45                                                        |  |
| Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Pro Gly Asp Gly Pro |  |
| 50 55 60                                                        |  |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Pro | Gly | Pro | Arg | Arg | Val | Pro | Ala | Cys | Phe | Arg | Leu | Glu | Gly | Xaa |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Glu | Pro | Ser | Arg | Ala | Leu | Pro | Gly | Arg | Leu | Thr | Ala | Gln | Leu | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 6...299
- (D) OTHER INFORMATION:
  
- (A) NAME/KEY: Modified Base
- (B) LOCATION: 43...43
- (D) OTHER INFORMATION: Xaa is Ala
  
- (A) NAME/KEY: Modified Base
- (B) LOCATION: 80...80
- (D) OTHER INFORMATION: Xaa is Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTGGA ATG AAG GCG GTG GGG GCC TGG CTC CTC TGC CTG CTG CTG CTG GGC | 50  |
| Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly       |     |
| 1 5 10 15                                                         |     |
| CTG GCC CTG CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG   | 98  |
| Leu Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu   |     |
| 20 25 30                                                          |     |
| ATC CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC GCR GGC CGT GGG ATC   | 146 |
| Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Gly Arg Gly Ile   |     |
| 35 40 45                                                          |     |
| CGG CCC GTG GGC CGC TTC GGC CGG CGA AGA GCT GCC CTG GGG GAC GGA   | 194 |
| Arg Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Leu Gly Asp Gly   |     |
| 50 55 60                                                          |     |
| CCC AGG CCT GGC CCC CGG CGT GTG CCG GCC TGC TTC CGC CTG GAA GGC   | 242 |
| Pro Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly   |     |
| 65 70 75                                                          |     |
| GGY GCT GAG CCC TCC CGA GCC CTC CCG GGG CGG CTG ACG GCC CAG CTG   | 290 |
| Xaa Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu   |     |
| 80 85 90 95                                                       |     |
| GTC CAG GAA TAACAGCGGG AGCCTGCCCC CCACCCCTCC TCCTCCACCA GCCACCTTC | 348 |
| Val Gln Glu                                                       |     |

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (ix) FEATURE:

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 43...43
- (D) OTHER INFORMATION: Xaa is Ala

- (A) NAME/KEY: Modified Base
- (B) LOCATION: 80...80
- (D) OTHER INFORMATION: Xaa is Gly

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |         |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---------|
| Met | Lys | Ala | Val | Gly | Ala | Trp | Leu | Leu | Cys | Leu | Leu | Leu | Gly | Leu     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |         |
| Ala | Leu | Gln | Gly | Ala | Ala | Ser | Arg | Ala | His | Gln | His | Ser | Met | Glu Ile |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |         |
| Arg | Thr | Pro | Asp | Ile | Asn | Pro | Ala | Trp | Tyr | Xaa | Gly | Arg | Gly | Ile Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |         |
| Pro | Val | Gly | Arg | Phe | Gly | Arg | Arg | Arg | Ala | Ala | Leu | Gly | Asp | Gly Pro |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |         |
| Arg | Pro | Gly | Pro | Arg | Arg | Val | Pro | Ala | Cys | Phe | Arg | Leu | Glu | Gly Xaa |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |         |
| Ala | Glu | Pro | Ser | Arg | Ala | Leu | Pro | Gly | Arg | Leu | Thr | Ala | Gln | Leu Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |         |
| Gln | Glu |     |     |     |     |     |     |     |     |     |     |     |     |         |

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| ATGAAGGCGG | TGGGGGCCTG | GCTCCTCTGC | CTGCTGCTGC | TGGGCCTGGC  | CCTGCAGGGG | 60  |
| GCTGCCAGCA | GAGCCACCA  | GCACTCCATG | GAGATCCGCA | GTGAGTGTCT  | AGCCCCGCCC | 120 |
| CTGCCCCCAG | GGGTCACAGG | GGGGGCCTGG | CCACTTCCTG | GGCTGGGACA  | TCCTTGCTAA | 180 |
| GCATCCTGGG | GTTGGGGTTT | GGCCTCCTGT | TCCCCAGACC | CTTCCCCCAG  | GTGGCCCGGA | 240 |
| CAGGTGCTCC | CAAGGGTCCC | GGCCCAGCAC | ACGGGGGAGG | GTCACCTCCTC | ACCACACGGG | 300 |
| TGGCCTGGGG | CTGAGTGCAC | GTCACCCATG | AGAACGGGGC | TGTGAGGACA  | GGAAAGGAAG | 360 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGGAGTGTGT | CCTGGTGTGA | GTCTGAAATC | CTACTTCCCA | AAGCCACCCC | AGCACCAGAA | 420 |
| ATGGGCGCTC | CGGGTGAACC | TCCTGTGCGG | GTGGGTGGTC | CTGGCATGGC | CTGGGCGACA | 480 |
| GGCAGCCATG | AGCTGAGCAC | ACACCCGGCC | CGGCCACCAG | GGCTGTATGC | TCCAGGGCAC | 540 |
| AGGCCTCCAT | GCGCTCTTCT | CTCTCTTTCC | AGCCCCCGAC | ATCAACCCTG | CCTGGTACGC | 600 |
| AGGCCGTGGG | ATCCGGCCCG | TGGGCCGCTT | CGGCCGGCGA | AGAGCTGCCC | TGGGGGACGG | 660 |
| ACCCAGGCCT | GGCCCCCGGC | GTGTGCCGGC | CTGCTTCCGC | CTGGAAGGCG | GTGCTGAGCC | 720 |
| CTCCCGAGCC | CTCCCGGGGC | GGCTGACGGC | CCAGCTGGTC | CAGGAATAA  |            | 769 |

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| ATGAAGGCGG | TGGGGGCCTG | GCTCCTCTGC | CTGCTGCTGC  | TGGGCCTGGC | CCTGCAGGGG | 60  |
| GCTGCCAGCA | GAGCCCACCA | GCACTCCATG | GAGATCCGCA  | GTGAGTGTCT | AGCCCCGCCC | 120 |
| CTGCCCCCAG | GGGTCACAGG | GGGGGCCTGG | CCACTTCCCTG | GGCTGGGACA | TCCTTGCTAA | 180 |
| GCATCCTGGG | GTTGGGGTTT | GGCCTCCTGT | TCCCCAGACC  | CTTCCCCCAG | GTGGCCCGGA | 240 |
| CAGGTGCTCC | CAAGGGTCCC | GGCCCAGCAC | ACGGGGGAGG  | GTCACTCCTC | ACCACACGGG | 300 |
| TGGCCTGGGG | CTGAGTGAC  | GTCACCCATG | AGAACGGGGC  | TGTGAGGACA | GGAAAGGAAG | 360 |
| GGGAGTGTGT | CCTGGTGTGA | GTCTGAAATC | CTACTTCCCA  | AAGCCACCCC | AGCACCAGAA | 420 |
| ATGGGCGCTC | CGGGTGAACC | TCCTGTGCGG | GTGGGTGGTC  | CTGGCATGGC | CTGGGCGACA | 480 |
| GGCAGCCATG | AGCTGAGCAC | ACACCCGGCC | CGGCCACCAG  | GGCTGTATGC | TCCAGGGCAC | 540 |
| AGGCCTCCAT | GCGCTCTTCT | CTCTCTTTCC | AGCCCCCGAC  | ATCAACCCTG | CCTGGTACGC | 600 |
| AGGCCGTGGG | ATCCGGCCCG | TGGGCCGCTT | CGGCCGGCGA  | AGAGCTGCCC | TGGGGGACGG | 660 |
| ACCCAGGCCT | GGCCCCCGGC | GTGTGCCGGC | CTGCTTCCGC  | CTGGAAGGCG | GTGCTGAGCC | 720 |
| CTCCCGAGCC | CTCCCGGGGC | GGCTGACGGC | CCAGCTGGTC  | CAGGAATAA  |            | 769 |

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ATGAAGGCGG | TGGGGGCCTG | GCTCCTCTGC | CTGCTGCTGC | TGGGCCTGGC | CCTGCAGGGG | 60  |
| GCTGCCAGCA | GAGCCCACCA | GCACTCCATG | GAGATCCGCA | CCCCCGACAT | CAACCCTGCC | 120 |
| TGGTACGCGG | GCCGTGGGAT | CCGGCCCGTG | GGCCGCTTCG | GCCGGCGAAG | AGCTGCCCCG | 180 |
| GGGGACGGAC | CCAGGCCTGG | CCCCCGGCGT | GTGCCGGCCT | GCTTCCGCCT | GGAAGGCGGG | 240 |
| GCTGAGCCCT | CCCAGCCCT  | CCCGGGGCGG | CTGACGGCCC | AGCTGGTCCA | GGAATAA    | 297 |

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...294  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG AAG GCG GTG GGG GCC TGG CTC CTC TGC CTG CTG CTG CTG GGC CTG | 48  |
| Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu |     |
| 1 5 10 15                                                       |     |
| GCC CTG CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG ATC | 96  |
| Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile |     |
| 20 25 30                                                        |     |
| CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC GCA GGC CGT GGG ATC CGG | 144 |
| Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg |     |
| 35 40 45                                                        |     |
| CCC GTG GGC CGC TTC GGC CGG CGA AGA GCT GCC CTG GGG GAC GGA CCC | 192 |
| Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Leu Gly Asp Gly Pro |     |
| 50 55 60                                                        |     |
| AGG CCT GGC CCC CGG CGT GTG CCG GCC TGC TTC CGC CTG GAA GGC GGT | 240 |
| Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly |     |
| 65 70 75 80                                                     |     |
| GCT GAG CCC TCC CGA GCC CTC CCG GGG CGG CTG ACG GCC CAG CTG GTC | 288 |
| Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val |     |
| 85 90 95                                                        |     |
| CAG GAA TAA                                                     | 297 |
| Gln Glu                                                         |     |

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

|                                                                 |
|-----------------------------------------------------------------|
| Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu |
| 1 5 10 15                                                       |
| Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile |
| 20 25 30                                                        |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Pro | Asp | Ile | Asn | Pro | Ala | Trp | Tyr | Ala | Gly | Arg | Gly | Ile | Arg |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Val | Gly | Arg | Phe | Gly | Arg | Arg | Arg | Ala | Ala | Leu | Gly | Asp | Gly | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Pro | Gly | Pro | Arg | Arg | Val | Pro | Ala | Cys | Phe | Arg | Leu | Glu | Gly | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Glu | Pro | Ser | Arg | Ala | Leu | Pro | Gly | Arg | Leu | Thr | Ala | Gln | Leu | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gln | Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24...272
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGCATCATCC AGGAAGACGG AGC ATG GCC CTG AAG ACG TGG CTT CTG TGC TTG | 53  |
| Met Ala Leu Lys Thr Trp Leu Leu Cys Leu                           |     |
| 1 5 10                                                            |     |
| CTG CTG CTA AGC TTG GTC CTC CCA GGG GCT TCC AGC CGA GCC CAC CAG   | 101 |
| Leu Leu Leu Ser Leu Val Leu Pro Gly Ala Ser Ser Arg Ala His Gln   |     |
| 15 20 25                                                          |     |
| CAC TCC ATG GAG ACA AGA ACC CCT GAT ATC AAT CCT GCC TGG TAC ACG   | 149 |
| His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr   |     |
| 30 35 40                                                          |     |
| GGC CGC GGG ATC AGG CCT GTG GGC CGC TTC GGC AGG AGA AGG GCA ACC   | 197 |
| Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Thr   |     |
| 45 50 55                                                          |     |
| CCG AGG GAT GTC ACT GGA CTT GGC CAA CTC AGC TGC CTC CCA CTG GAT   | 245 |
| Pro Arg Asp Val Thr Gly Leu Gly Gln Leu Ser Cys Leu Pro Leu Asp   |     |
| 60 65 70                                                          |     |
| GGA CGC ACC AAG TTC TCT CAG CGT GGA TAACACCCCA GCTCGAGAAG ACAGTGC | 299 |
| Gly Arg Thr Lys Phe Ser Gln Arg Gly                               |     |
| 75 80                                                             |     |
| TGCTGAGCCC AAGCCACAC TCCCTGTCCC CTGCAGACCC TCCTCTACCC TCCCTCTCCT  | 359 |
| CTGCT                                                             | 364 |

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Lys | Thr | Trp | Leu | Leu | Cys | Leu | Leu | Leu | Leu | Ser | Leu | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Pro | Gly | Ala | Ser | Ser | Arg | Ala | His | Gln | His | Ser | Met | Glu | Thr | Arg |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Thr | Pro | Asp | Ile | Asn | Pro | Ala | Trp | Tyr | Thr | Gly | Arg | Gly | Ile | Arg | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Gly | Arg | Phe | Gly | Arg | Arg | Arg | Ala | Thr | Pro | Arg | Asp | Val | Thr | Gly |
|     | 50  |     |     |     | 55  |     |     | 60  |     |     |     |     |     |     |     |
| Leu | Gly | Gln | Leu | Ser | Cys | Leu | Pro | Leu | Asp | Gly | Arg | Thr | Lys | Phe | Ser |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Gln | Arg | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...297
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gtg | ggc | atg | gtg | ggc | aac | gtc | ctg | ctg | gtg | ctg | gtg | atc | gcg | cgg | gtg | 48  |
| Val | Gly | Met | Val | Gly | Asn | Val | Leu | Leu | Val | Leu | Val | Ile | Ala | Arg | Val |     |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     |
| cgc | cgg | ctg | cac | aac | gtg | acg | aac | ttc | ctc | atc | ggc | aac | ctg | gcc | ttg | 96  |
| Arg | Arg | Leu | His | Asn | Val | Thr | Asn | Phe | Leu | Ile | Gly | Asn | Leu | Ala | Leu |     |
|     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |     |
| tcc | gac | gtg | ctc | atg | tgc | acc | gcc | tgc | gtg | ccg | ctc | acg | ctg | gcc | tat | 144 |
| Ser | Asp | Val | Leu | Met | Cys | Thr | Ala | Cys | Val | Pro | Leu | Thr | Leu | Ala | Tyr |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| gcc | ttc | gag | cca | cgc | ggc | tgg | gtg | ttc | ggc | ggc | ggc | ctg | tgc | cac | ctg | 192 |
| Ala | Phe | Glu | Pro | Arg | Gly | Trp | Val | Phe | Gly | Gly | Gly | Leu | Cys | His | Leu |     |
|     | 50  |     |     |     | 55  |     |     | 60  |     |     |     |     |     |     |     |     |
| gtc | ttc | ttc | ctg | cag | ccg | gtc | acc | gtc | tat | gtg | tcg | gtg | ttc | acg | ctc | 240 |

Val Phe Phe Leu Gln Pro Val Thr Val Tyr Val Ser Val Phe Thr Leu  
65 70 75 80

acc acc atc gca gtg gac cgg tac gtc gtg ctg gtg cac ccg ctg agg 288  
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg  
85 90 95

cgg cgc atc 297  
Arg Arg Ile

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val  
1 5 10 15  
Arg Arg Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu  
20 25 30  
Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr  
35 40 45  
Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Gly Leu Cys His Leu  
50 55 60  
Val Phe Phe Leu Gln Pro Val Thr Val Tyr Val Ser Val Phe Thr Leu  
65 70 75 80  
Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg  
85 90 95  
Arg Arg Ile

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...204
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ggc ctg ctg ctg gtc acc tac ctg ctc cct ctg ctg gtc atc ctc ctg 48  
Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu

| 1                                                               | 5 | 10 | 15 |     |
|-----------------------------------------------------------------|---|----|----|-----|
| tct tac gtc cgg gtg tca gtg aag ctc cgc aac cgc gtg gtg ccg ggc |   |    |    | 96  |
| Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly |   |    |    |     |
| 20                                                              |   | 25 | 30 |     |
| tgc gtg acc cag agc cag gcc gac tgg gac cgc gct cgg cgc cgg cgc |   |    |    | 144 |
| Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg |   |    |    |     |
| 35                                                              |   | 40 | 45 |     |
| acc ttc tgc ttg ctg gtg gtg gtc gtg gtg gtg ttt gcc atc tgc tgg |   |    |    | 192 |
| Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala Ile Cys Trp |   |    |    |     |
| 50                                                              |   | 55 | 60 |     |
| ttg cct tac tac                                                 |   |    |    | 204 |
| Leu Pro Tyr Tyr                                                 |   |    |    |     |
| 65                                                              |   |    |    |     |

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Leu | Leu | Val | Thr | Tyr | Leu | Leu | Pro | Leu | Leu | Val | Ile | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Tyr | Val | Arg | Val | Ser | Val | Lys | Leu | Arg | Asn | Arg | Val | Val | Pro | Gly |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Cys | Val | Thr | Gln | Ser | Gln | Ala | Asp | Trp | Asp | Arg | Ala | Arg | Arg | Arg | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr | Phe | Cys | Leu | Leu | Val | Val | Val | Val | Val | Val | Phe | Ala | Ile | Cys | Trp |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Leu | Pro | Tyr | Tyr |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Met | Val | Gly | Asn | Val | Leu | Leu | Val | Leu | Val | Ile | Ala | Arg | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Leu | His | Asn | Val | Thr | Asn | Phe | Leu | Ile | Gly | Asn | Leu | Ala | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Asp | Val | Leu | Met | Cys | Thr | Ala | Cys | Val | Pro | Leu | Thr | Leu | Ala | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Phe | Glu | Pro | Arg | Gly | Trp | Val | Phe | Gly | Gly | Gly | Leu | Cys | His | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Phe | Phe | Leu | Gln | Pro | Val | Thr | Val | Tyr | Val | Ser | Val | Phe | Thr | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Thr | Thr | Ile | Ala | Val | Asp | Arg | Tyr | Val | Val | Leu | Val | His | Pro | Leu | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Arg | Ile | Gly | Leu | Leu | Leu | Val | Thr | Tyr | Tyr | Leu | Leu | Pro | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ile | Leu | Leu | Ser | Tyr | Val | Arg | Val | Ser | Val | Lys | Leu | Arg | Asn | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Val | Pro | Gly | Cys | Val | Thr | Gln | Ser | Gln | Ala | Asp | Trp | Asp | Arg | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Arg | Arg | Arg | Thr | Phe | Cys | Leu | Leu | Val | Val | Val | Val | Val | Val | Phe |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Ala | Ile | Cys | Trp | Leu | Pro | Tyr | Tyr |     |     |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Val | Ser | Gly | Asn | Leu | Ala | Leu | Ile | Ile | Ile | Ile | Leu | Lys | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Glu | Met | Arg | Asn | Val | Thr | Asn | Ile | Leu | Ile | Val | Asn | Leu | Ser | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Asp | Leu | Leu | Val | Ala | Val | Met | Cys | Leu | Pro | Phe | Thr | Phe | Val | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Leu | Met | Asp | His | Trp | Val | Phe | Gly | Glu | Thr | Met | Cys | Lys | Leu | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Phe | Val | Gln | Cys | Val | Ser | Ile | Thr | Val | Ser | Ile | Phe | Ser | Leu | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Leu | Ile | Ala | Val | Glu | Arg | His | Gln | Leu | Ile | Ile | Asn | Pro | Arg | Gly | Trp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Pro | Asn | Asn | Arg | His | Ala | Tyr | Ile | Gly | Ile | Thr | Val | Ile | Trp | Val |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ala | Val | Ala | Ser | Ser | Leu | Pro | Phe | Val | Ile | Tyr | Gln | Ile | Leu | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Glu | Pro | Phe | Gln | Asn | Val | Ser | Leu | Ala | Ala | Phe | Lys | Asp | Lys | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Cys | Phe | Asp | Lys | Phe | Pro | Ser | Asp | Ser | His | Arg | Leu | Ser | Tyr | Thr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |

Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys Phe Ile Phe  
165 170 175  
Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg Arg Asn Asn Met  
180 185 190  
Met Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Glu Thr Lys Arg  
195 200 205  
Ile Asn Val Met Leu Leu Ser Ile Val Val Ala Phe Ala Val Cys Trp  
210 215 220  
Leu Pro Leu Thr  
225

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu  
1 5 10 15  
Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile  
20 25 30  
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg  
35 40 45  
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Pro Gly Asp Gly Pro  
50 55 60  
Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly  
65 70 75 80  
Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val  
85 90 95  
Gln Glu

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

gtggaatgaa ggcggtgggg gcctggctcc tctgcctgct gctgctgggc ctggccctgc 60  
agggggctgc cagcagagcc caccagcact ccatggagat ccgcaccccc gacatcaacc 120  
ctgcctggta cgcgggcccgt gggatccggc ccgtgggccg cttcggcccg cgaagagctg 180  
ccccggggga cggacccagg cctggccccc ggctgtgtcc ggctgtcttc cgcctggaag 240  
gcggcgctga gccctcccga gccctcccgg ggcggtgac ggcccagctg gtccaggaat 300  
aacagcggga gcctgcccc caccctcct cctccaccag ccaccttccc tccagtccta 360  
ataaaagcag ctggcttgtt 380

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ggcatcatcc aggaagacgg agcatggccc tgaagacgtg gcttctgtgc ttgctgctgc | 60  |
| taagcttggc cctcccaggg gcttcaagcc gagcccacca gcactccatg gagacaagaa | 120 |
| cccctgatat caatcctgcc tggtagacgg gccgcgggat caggcctgtg ggccgcttcg | 180 |
| gcaggagaag ggcaaccccg agggatgtca ctggacttgg ccaactcagc tgccctccac | 240 |
| tggatggacg caccaagttc tctcagcgtg gataacaccc cagctcgaga agacagtgtc | 300 |
| gctgagccca agcccacact ccctgtcccc tgcagaccct cctctaccct ccctctcctc | 360 |
| tgct                                                              | 364 |

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24..284
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ggcctcctcg gaggagccaa ggg atg aag gtg ctg agg gcc tgg ctc ctg tgc | 53  |
| Met Lys Val Leu Arg Ala Trp Leu Leu Cys                           |     |
| 1 5 10                                                            |     |
| ctg ctg atg ctg ggc ctg gcc ctg cgg gga gct gca agt cgt acc cat   | 101 |
| Leu Leu Met Leu Gly Leu Ala Leu Arg Gly Ala Ala Ser Arg Thr His   |     |
| 15 20 25                                                          |     |
| cgg cac tcc atg gag atc cgc acc cct gac atc aat cct gcc tgg tac   | 149 |
| Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr   |     |
| 30 35 40                                                          |     |
| gcc agt cgc ggg atc agg cct gtg ggc cgc ttc ggt cgg agg agg gca   | 197 |
| Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly Arg Arg Arg Ala   |     |
| 45 50 55                                                          |     |
| acc ctg ggg gac gtc ccc aag cct ggc ctg cga ccc cgg ctg acc tgc   | 245 |
| Thr Leu Gly Asp Val Pro Lys Pro Gly Leu Arg Pro Arg Leu Thr Cys   |     |
| 60 65 70                                                          |     |

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ttc ccc ctg gaa ggc ggt gct atg tcg tcc cag gat ggc tgacagccag 294
Phe Pro Leu Glu Gly Gly Ala Met Ser Ser Gln Asp Gly
 75 80 85

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ala | Val | Gly | Ala | Trp | Leu | Leu | Cys | Leu | Leu | Leu | Leu | Gly | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Gln | Gly | Ala | Ala | Ser | Arg | Ala | His | Gln | His | Ser | Met | Glu | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Thr | Pro | Asp | Ile | Asn | Pro | Ala | Trp | Tyr | Ala | Gly | Arg | Gly | Ile | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Val | Gly | Arg | Phe | Gly | Arg | Arg | Arg | Ala | Ala | Pro | Gly | Asp | Gly | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Pro | Gly | Pro | Arg | Arg | Val | Pro | Ala | Cys | Arg | Phe | Leu | Glu | Gly | Gly |



(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1110
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| atg acc tca ctg ccc cct gga acc act ggg gac ccc gat ttg ttt tct | 48  |
| Met Thr Ser Leu Pro Pro Gly Thr Thr Gly Asp Pro Asp Leu Phe Ser |     |
| 1 5 10 15                                                       |     |
| ggg ccg tcg cca gcc ggc tcc act cca gcc aac cag agt gca gag gct | 96  |
| Gly Pro Ser Pro Ala Gly Ser Thr Pro Ala Asn Gln Ser Ala Glu Ala |     |
| 20 25 30                                                        |     |
| tca gag agc aat gtg tct gcg acg gtt ccc aga gct gca gca gtc acg | 144 |
| Ser Glu Ser Asn Val Ser Ala Thr Val Pro Arg Ala Ala Ala Val Thr |     |
| 35 40 45                                                        |     |
| ccg ttc cag agc ctg caa cta gtg cac cag ctg aag gca ctg atc gtg | 192 |
| Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Ala Leu Ile Val |     |
| 50 55 60                                                        |     |
| atg ctg tac agc atc gtg gtg gtc gtg ggt ctg gtg ggc aac tgc ctt | 240 |
| Met Leu Tyr Ser Ile Val Val Val Val Gly Leu Val Gly Asn Cys Leu |     |
| 65 70 75 80                                                     |     |
| ctt gtg ctg gtg atc gcg cgc gtg cgc cgg ctg cac aac gtg acc aac | 288 |
| Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn |     |
| 85 90 95                                                        |     |
| ttc ctc atc ggc aac ctg gcc ttg tcc gat gtg ctc atg tgt gcc gcc | 336 |
| Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Ala Ala |     |
| 100 105 110                                                     |     |
| tgt gtg cct ctc acg ctg gcc tac gcc ttt gaa cct cgt ggc tgg gtg | 384 |
| Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val |     |
| 115 120 125                                                     |     |
| ttc ggt gga ggc ctg tgc cac ctt gtt ttc ttc ctg cag ccg gtc acc | 432 |
| Phe Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr     |     |
| 130 135 140                                                     |     |
| gtc tac gta tcg gtg ttc aca ctc acc aca atc gct gtg gac cgc tat | 480 |
| Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr |     |
| 145 150 155 160                                                 |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| gtg gtt ctg gtg cac ccg cta cgt cgg cgc att tca ctg aag ctc agc<br>Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Lys Leu Ser<br>165 170 175     | 528  |
| gcc tac gct gtg ctg ggc atc tgg gct cta tct gca gtg ctg gcg ctg<br>Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu<br>180 185 190     | 576  |
| ccg gcc gcg gtg cac acc tac cat gta gag ctc aag ccc cac gac gtg<br>Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val<br>195 200 205     | 624  |
| cgc ctc tgc gag gag ttc tgg ggt tgc cag gag cgc cag cga cag atc<br>Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile<br>210 215 220     | 672  |
| tat gcc tgg ggg ctg ctg ctg ggc acc tat ttg ctc ccc ctg ctg gcc<br>Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala<br>225 230 235 240 | 720  |
| att ctc ctg tct tac gtc cgg gtg tgc gtg aag ttg cgg aac cgc gtg<br>Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val<br>245 250 255     | 768  |
| gtg cct ggc agc gtg acc cag agc cag gct gac tgg gac cga gcg cgt<br>Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg<br>260 265 270     | 816  |
| cgc cgt cgc act ttc tgc ctg ctg gtg gtg gtg gtg gtc gtg ttc gcg<br>Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala<br>275 280 285     | 864  |
| gtc tgc tgg ctg cct ctg cac att ttc aac ctg ctg cgg gac ctg gac<br>Val Cys Trp Leu Pro Leu His Ile Phe Asn Leu Leu Arg Asp Leu Asp<br>290 295 300     | 912  |
| ccg cgt gcc atc gac ccc tac gcc ttc ggg ctg gtg cag ctc ctc tgc<br>Pro Arg Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys<br>305 310 315 320 | 960  |
| cac tgg ctt gcc atg agc tcc gcc tgc tac aac ccc ttc atc tat gcg<br>His Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala<br>325 330 335     | 1008 |
| tcg ctg cac gac agc ttc cga gag gag cta cgc aag atg ctt ctg tct<br>Ser Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Met Leu Leu Ser<br>340 345 350     | 1056 |
| tgg ccc cgc aag atc gtg cct cat ggc cag aat atg acc gtc agt gtg<br>Trp Pro Arg Lys Ile Val Pro His Gly Gln Asn Met Thr Val Ser Val<br>355 360 365     | 1104 |
| gtc atc tgatga<br>Val Ile<br>370                                                                                                                      | 1116 |

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ser | Leu | Pro | Pro | Gly | Thr | Thr | Gly | Asp | Pro | Asp | Leu | Phe | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Pro | Ser | Pro | Ala | Gly | Ser | Thr | Pro | Ala | Asn | Gln | Ser | Ala | Glu | Ala |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Glu | Ser | Asn | Val | Ser | Ala | Thr | Val | Pro | Arg | Ala | Ala | Ala | Val | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Phe | Gln | Ser | Leu | Gln | Leu | Val | His | Gln | Leu | Lys | Ala | Leu | Ile | Val |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Met | Leu | Tyr | Ser | Ile | Val | Val | Val | Val | Gly | Leu | Val | Gly | Asn | Cys | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Val | Leu | Val | Ile | Ala | Arg | Val | Arg | Arg | Leu | His | Asn | Val | Thr | Asn |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Leu | Ile | Gly | Asn | Leu | Ala | Leu | Ser | Asp | Val | Leu | Met | Cys | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Val | Pro | Leu | Thr | Leu | Ala | Tyr | Ala | Phe | Glu | Pro | Arg | Gly | Trp | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Gly | Gly | Gly | Leu | Cys | His | Leu | Val | Phe | Phe | Leu | Gln | Pro | Val | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Tyr | Val | Ser | Val | Phe | Thr | Leu | Thr | Thr | Ile | Ala | Val | Asp | Arg | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Val | Leu | Val | His | Pro | Leu | Arg | Arg | Arg | Ile | Ser | Leu | Lys | Leu | Ser |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Tyr | Ala | Val | Leu | Gly | Ile | Trp | Ala | Leu | Ser | Ala | Val | Leu | Ala | Leu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Pro | Ala | Ala | Val | His | Thr | Tyr | His | Val | Glu | Leu | Lys | Pro | His | Asp | Val |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Arg | Leu | Cys | Glu | Glu | Phe | Trp | Gly | Ser | Gln | Glu | Arg | Gln | Arg | Gln | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Tyr | Ala | Trp | Gly | Leu | Leu | Leu | Gly | Thr | Tyr | Leu | Leu | Pro | Leu | Leu | Ala |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Ile | Leu | Leu | Ser | Tyr | Val | Arg | Val | Ser | Val | Lys | Leu | Arg | Asn | Arg | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Val | Pro | Gly | Ser | Val | Thr | Gln | Ser | Gln | Ala | Asp | Trp | Asp | Arg | Ala | Arg |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Arg | Arg | Arg | Thr | Phe | Cys | Leu | Leu | Val | Val | Val | Val | Val | Val | Phe | Ala |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Val | Cys | Trp | Leu | Pro | Leu | His | Ile | Phe | Asn | Leu | Leu | Arg | Asp | Leu | Asp |
|     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Pro | Arg | Ala | Ile | Asp | Pro | Tyr | Ala | Phe | Gly | Leu | Val | Gln | Leu | Leu | Cys |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| His | Trp | Leu | Ala | Met | Ser | Ser | Ala | Cys | Tyr | Asn | Pro | Phe | Ile | Tyr | Ala |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |



[illegible]